

Link Prediction in Social Networks

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Certificate

This is to certify that the thesis entitled, ***LINK PREDICTION IN SOCIAL NETWORKS*** submitted by ***SHAKTISRI ANILRANJAN SAHOO (109CS0184)*** in partial fulfillment of the requirements for the completion of Bachelor of Technology Degree in Computer Science and Engineering at the National Institute of Technology, Rourkela is an authentic work carried out by him under my supervision and guidance . To the best of my knowledge, Neither this thesis or any part of it has been submitted for any degree or diploma award elsewhere.

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Acknowledgment

With great satisfaction and pride I present my thesis on the project under the Research Project paper during final Year, for partial fulfillment of my Bachelor of Technology degree in Computer Science and Engineering at NIT Rourkela.

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Abstract

In a social network there can be many different kind of links or edges between the nodes. Those could for example be social contacts, hyper-references or phone-calls. Link Prediction is the problem of predicting edges that either don't yet exist at the given time t or exist, but have not been discovered, are likely to occur in the near future. We develop approaches to link prediction based on measures for analysing the proximity of nodes in a network. Consider a co-authorship network among scientists, e.g. two scientists who are close in the network will have colleagues in common, so they are more likely to collaborate in the near future. Our goal is to make this intuitive notion precise and to understand which measures of proximity in a network lead to the most accurate link predictions. Link prediction algorithms can be classified into three categories: Node neighborhood approaches, Path based approaches and Meta approaches. Node neighborhood approach is based on local features of a network, focusing mainly on the nodes structure(i.e. based on the number of common friends that two users share). The local-based measures are: Common Neighbors, Jaccards coefficient, Adamic/Adar and Preferential Attachment. Path based algorithms considers the ensemble of all paths between two nodes. The Path based algorithms are: Katz, Sim-Rank, Hitting Time and Commute Time, Rooted PageRank, PropFlow and High-Performance Link Prediction. Meta-Approaches alter the data before being passed to one of the path based approaches. The algorithms are: Low-rank approximation, Unseen bigrams and Clustering.

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Chapter 1

Introduction

1.1 Introduction to Social Networks

A Social Structure consists of nodes(Individuals or Organizations) and nodes are connected by different types of relationships. A set of social actors or nodes(such as individuals or organizations) and a set of the dyadic ties between these nodes constitute a social network. For example scientists in a discipline, employees in a large company, business leaders can be thought as nodes in a network and co-authors of a paper, working on a project, serve together on board can be thought as edges respectively. The idea behind Social Networks is to create opportunities to develop friendships, share information and promote business in a network. OSN like Facebook and Twitter have become important part of daily life of millions of people. The enormous growth and dynamics of these networks has led to several researches that examine the network properties i.e. structural and behavioural properties of large scale social networks.

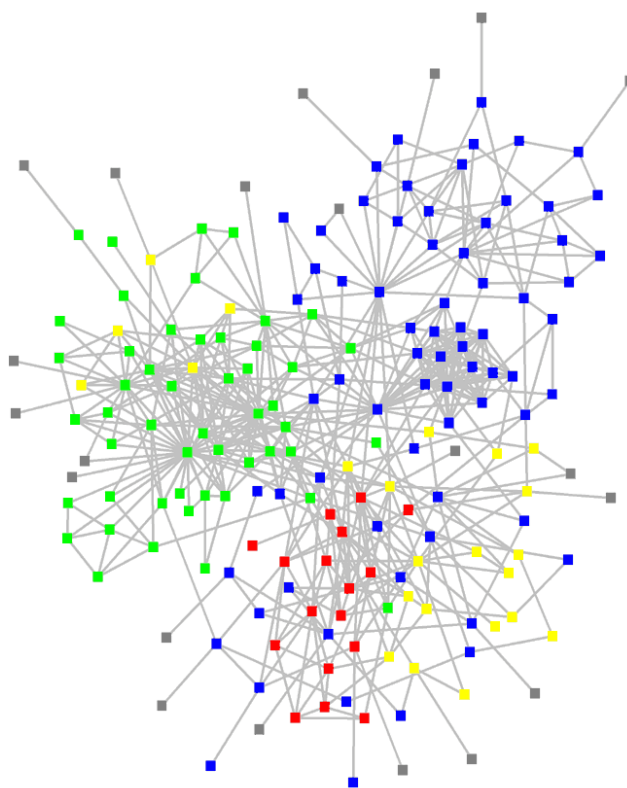


FIGURE 1.1: Social Network

1.2 Social Network Analysis

Social network analysis(SNA) is in depth analysis of social networks. SNA is the mapping and measuring of relationships, links and flows between nodes(people, groups, organizations, computers) and many other connected entities which provides some knowledge and information. The vertices or nodes in the network are the people and groups while the links show relationships or flows between the nodes. We can do visual and a mathematical analysis of human relationships through SNA that helps us to make sense out of the social network, to find the complex structure of social networks, to understand the evolution of social networks, network dynamics and to discover complex communication patterns and characteristic features of the network.

1.3 Tasks Of Social Network Analysis

Social networks are dynamic by nature. They change very quickly over a specific interval. Continuously new relationships establish between nodes and many old relationships break. These relational changes(when people become friends through common friends), characteristics of the nodes, characteristics of pairs of actors or link weights and random unexplained events influences the graph characteristics. The key tasks of SNA include different measures to rank nodes(or edges), Link prediction problem, Inferring social networks from social events, Viral marketing, Community detection, Design of incentives in networks, Determining implicit social hierarchy, Network formation, Sparsication of social networks(with purpose). There are many measures to rank nodes like degree centrality, closeness centrality, clustering coefficient, betweenness centrality, Katz centrality and Eigen vector centrality. Link prediction is predicting the links that does not exist or exist, but not known and have probability to occur in the near future. Viral marketing deals with exploiting social connectivity patterns of users to propagate the awareness of product. Community detection involves graph partitioning based on activities over the social network and determining the dense sub graphs in a social network. In designing the incentives, only the person who answers the query is rewarded, with no reward for the intermediaries. Since individuals are often rational and intelligent, they may not participate in answering the queries unless

some kind of incentives are provided. SNA has many applications like information sharing, Information sharing, Understand the spread of diseases, Marketing in e-Commerce and e-Business, determine the influential entities, build effective social and political campaign, Predict future events, tracking terrorists and location based crowdsourcing.

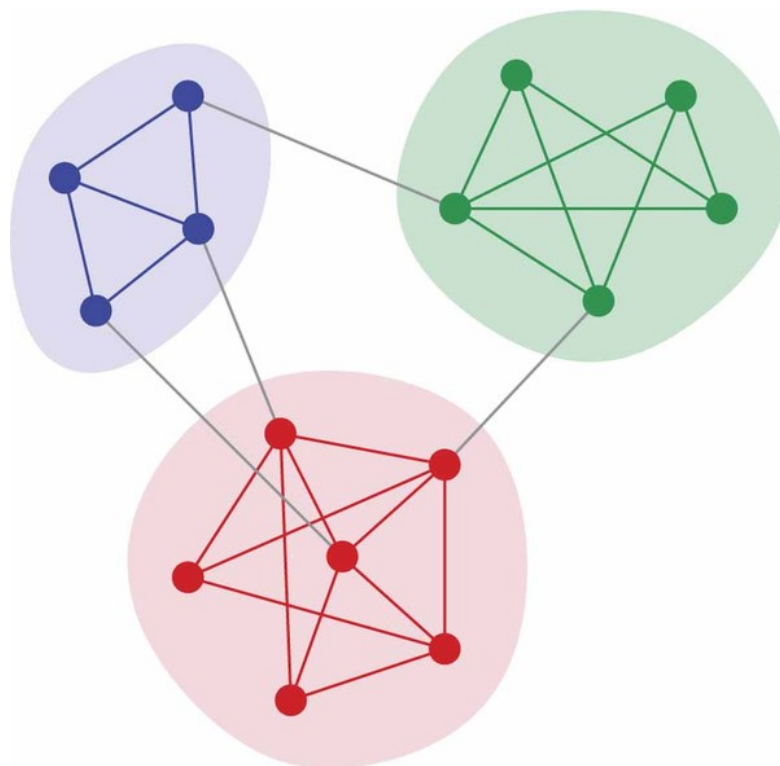


FIGURE 1.2: Community Detection in Social Networks

1.4 Link Prediction Problem

Different kind of links or edges between the nodes exist in a social network. For example, social contacts, phone-calls or hyper-references. On analysis of social networks, there can be many information about the linkage between the nodes that are not discovered or unknown at a given point of time. Link Prediction is the problem of predicting links that either don't yet exist at the given time t or exist, but unknown up to this time. Given a picture of a social network (nodes and links) at time t , we need to predict accurately the links that will be added to the network during the interval from time t to a given future time $t+1$. In effect, the link prediction problem concentrates on to what extent can the evolution of a social network be modelled by using intrinsic features of the network itself? Let

us consider a co-authorship network among researchers, for example, there are different reasons, outside to the network, why two researchers who have never written a paper together will do so in the next few years. Or, when one of the researchers changes institutions, they may come geographically very close. Such interactions are be hard to predict. But by studying the network characteristics, we can predict the possible links that are going to form. Our objective is to make this intuitive notion very exact, and to understand which measures of proximity in a graph lead to accurate predictions.

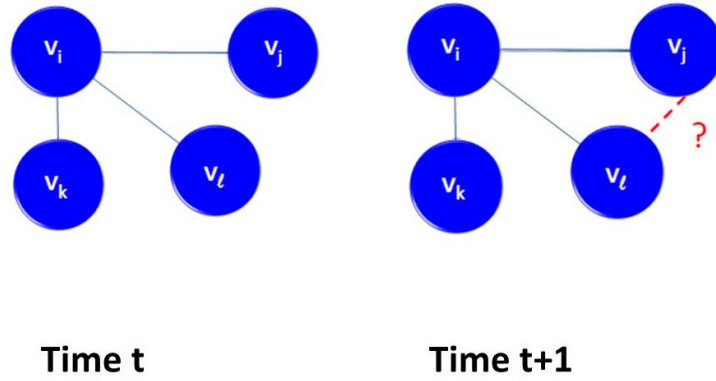


FIGURE 1.3: Link Prediction in Social Networks

The link prediction problem is also deals with the problem of getting missing links from a known network, in a number of fields. It involves prediction of additional links that are not directly visible currently, are likely to exist in a network based on observable data. It considers a static picture of the network, rather than taking network evolution and network dynamics. It also considers specific properties of the nodes in the network, rather than computing the power of prediction methods that focuses on the graph structure.

1.5 Application of Link Prediction

Apart from its role as a basic question in social network formation, the link prediction problem could be related to a number of interesting applications of social networks. It is found that a large and medium organisation like a company can benefit from the involvement within the social network among its employees. These benefits to supplement the organisation hierarchy defined by the organization. Effective and efficient methods for link prediction could be used to analyse and study such a social network, and suggest interactions that have not yet been

utilized within the organization, more likely to form. Link Prediction has a great role in security research, largely inspired by the problem of controlling terrorist networks and predicting their future involvement. In bioinformatics, efficient link prediction techniques can be used to predict interactions between proteins. In e-commerce it helps in building the recommendation systems so that helps in viral marketing and effective product awareness.

Chapter 2

Literature Review

Given a social network $G(V, E)$ in which an edge represents some kind of interactions between its vertices on nodes at a given time t . Suppose we have a snapshot of a social network at a given time. We choose four times $t_0 < t_{00} < t_1 < t_{01}$, and give our algorithm to predict links that are likely to be formed in the near future from the network $G[t_0; t_{00}]$. That results in predicting new links, not present in $G[t_0; t_{00}]$, that are expected to appear in the network $G[t_1; t_{01}]$. We refer to $[t_0; t_{00}]$ as the training interval and $[t_1; t_{01}]$ as the test interval [1].

The most basic approach for similarity between any pair of nodes is by taking the length of their shortest path in graph. We rank pairs of nodes in descending order of $score(x, y)$, where $score(x, y)$ is the negative of the shortest path length between x and y . We take a snapshot of a social network as training set and predict the interactions among the nodes of training set that are likely to occur in near future. The algorithms are classified as belows [2].

2.1 NODE NEIGHBORHOOD ALGORITHMS

Node neighborhood meaning the nodes directly connected to the two given nodes. It is simple technique which traverse only paths of length 2. For any node A it check the neighbors of neighbour of A and computes their similarity with A. It considers only local features of a network, focusing mainly on the nodes structure(i.e. based on the number of common friends that two users share).

2.1.1 Common Neighbors

The Common Neighbors method provide a measure for similarity by calculating the intersection of the sets of neighbors of the nodes to predict future linkage.

The Common Neighbors(CN) is defined as follows

$$CN(x, y) := \Gamma(x) * \Gamma(y)$$

This measurement is based on the idea that two nodes a and b have an increased probability to connect if they have a shared neighbor c . With a growing number of shared neighbors this probability grows even higher.

The weighted Common Neighbors(CNw) is defined as follows where $w(x, y)$ is the number of interactions between the nodes x and y .

$$CNw(x, y) := \sum_{z \in \Gamma(x) \cap \Gamma(y)} \frac{w(x, z) + w(y, z)}{2}$$

2.1.2 Jaccard coefficient

Jaccards coefficient measures number of the features(neighbors) that are shared between two nodes commensurate to all features that either one of the nodes has. Jaccards coefficient is a normalized variation of Common Neighbors [?]R7).

The Jacard coefficient is defined as follows

$$J(x, y) := \frac{|\Gamma(x) \cap \Gamma(y)|}{|\Gamma(x) \cup \Gamma(y)|}$$

This is the Common Neighbors measurement normalized by the union of the node neighborhoods.

2.1.3 Adamic/Adar

It is a measurement that compares how many attributes two nodes have in common. They rate items that are unique to a few users more heavily than items shared amongst a huge group of users. This measurement can easily be adjusted in the context of node neighborhood by looking at shared neighbors as an attribute. Therefore the sum over the shared neighbors inverse of the logarithms of their neighborhoods is proposed [3].

The Adamic/Adar is defined as follows

$$AA(x, y) := \sum_{z \in \Gamma(x) \cap \Gamma(y)} \frac{1}{\log|\Gamma(z)|}$$

The weighted Adamic/Adar (AAw) is defined as follows where $w(x; y)$ is the number of interactions between the nodes x and y [4].

$$AAw(x, y) := \sum_{z \in (x) \cap \Gamma(y)} \frac{w(x, z) + w(y, z)}{2} \cdot \frac{1}{\log \sum_{z' \in \Gamma(z)} w(z', z)}$$

2.1.4 Preferential Attachment

Preferential Attachment is based on the hypothesis that a node x will get new neighbors faster than a node y given y has less neighbors than x . So the probability that a node will form a new link varies with number of its present neighbors. The likelihood of two nodes being connected by an edge based on preferential attachment is measured by multiplying the number of their neighbors [5].

The Preferential Attachment is defined as follows

$$PA(x, y) := \Gamma(x) \cdot \Gamma(y)$$

The weighted Preferential Attachment (PAw) is defined as follows where $w(x, y)$ is the number of interactions between the nodes x and y :

$$PAw(x, y) := \sum_{x' \in \Gamma(x)} w(x, x') \cdot \Gamma_{y' \in \Gamma(y)} w(y', y)$$

2.2 PATH BASED ALGORITHMS

Some measurements of link prediction take all paths between two nodes in consideration. The computation of graphs that take the entire graph in consideration is by nature much more complex than node neighborhood algorithms.

2.2.1 Katz

A measurement that takes all paths between two nodes in consideration while rating short paths more heavily. The measurement exponentially reduce the contribution of a path to the measure in order to give less weightage longer paths. Therefore it uses a factor of β^l where l is the path length.

The Katz is defined as follows

$$K(x, y) := \sum_{l=1}^{\infty} \beta^l \cdot |paths_{x,y}^{<l>}|$$

where $paths_{x,y}^{<l>}$ the set of all paths from source x to destination y that have the path length l .

- Unweighted : $paths_{x,y}^{<l>} = 1$, if x and y have collaborated and 0 otherwise
- Weighted : $paths_{x,y}^{<l>}$ is the number of times that x and y have collaborated

The β can be used to control how much the length of the paths should be considered. A very small β concludes to an algorithm where paths of length three or more are taken much less into account and therefor the algorithm converges node neighborhood algorithms. It has roughly cubic complexity as it requires matrix inversion [6].

2.2.2 SimRank

If two nodes are referenced by more similar objects, then the two nodes have large similarity value. Every object obviously has a similarity score of 1 to itself. Node x and node y are then similar to the degree they are joined to similar neighbors [7].

The SimRank is defined as follows

$$S(x, x) := 1$$

$$S(x, y) := \gamma \cdot \frac{\sum_{a \in \Gamma(x)} \sum_{b \in \Gamma(y)} S(x, y)}{\Gamma(x) \cdot \Gamma(y)}$$

γ is a constant with $\gamma \in [0, 1]$. The constant can be thought of as a confidence level. If you consider a situation in which a and b are both neighbors to c , than obviously the similarity of c to itself is 1, but we do not want to conclude that $s(a, b) = s(c, c) = 1$. Instead we let $s(a, b) = \gamma * s(x, x)$ because we are not as confident about the similarity of a and b as we are about $s(x, x) = 1$.

2.2.3 Hitting Time and Commute Time

Starting from a node x a random walk on a given graph moves iteratively over the graph while choosing the next node each step at random. The expected number of steps to get from x to y via a random walk is defined as the Hitting Time $H(x, y)$. A short hitting time implies node similarity and therefore a heightened chance of future linking. The commute time $C(x, y)$ is a variant of Hitting time which is useful for undirected graphs, because the hitting time is not symmetric. Therefore it is defined as follows:

$$C(x, y) := H(x, y) + H(y, x)$$

The commute time can have high variance, hence, prediction by this feature can be poor. If z is a node with high stationary probability far off x and y , then a random walker would probably reach the neighborhood of z . To avoid that we can use reset the random walker to x with a fixed probability of α .

two normalized versions Hitting Time normalized (H_n) and Commute-Time normalized (C_n) are defined where π_x is the stationary probability of x to safeguard it against vertices with a very high π :

$$Hn(x, y) := -H(x, y) \cdot \pi_y$$

$$Cn(x, y) := -(H(x, y) \cdot \pi_y + H(y, x) \cdot \pi_x)$$

2.2.4 Rooted PageRank

Rooted PageRank is a modification of the Page Rank measure (which is an attribute of a single vertex) for link prediction. It is the amount of step from x to y with a probability of α to return to x each step (and $1 - \alpha$ to go to a random neighbor). This metric is asymmetric and can be made symmetric by summing with the counterpart where the role of x and y are reversed [8].

The rooted pagerank(RPR) between all node pairs is calculated as follows: Let D be a diagonal degree matrix defined as:

$$D[i, i] := \sum_j A[i, j]$$

And let N be the following matrix with normalized row sums.

$$N := D^{-1}$$

Then the Rooted Pagerank can be calculated as

$$RPR := (1 - \beta)(I - \beta N)^{-1}$$

2.2.5 PropFlow and High-Performance Link Prediction

The unsupervised PropFlow method calculates the probability that a random walker reaches node y from node x in l steps or fewer while using link weights as transition probabilities. If the algorithm revisits any node including x or if it reaches y the algorithm terminates. When compared to Rooted PageRank the algorithm is more localized and is insensitive to topologic noise far from the source node. It is faster to compute because it does not require random resets. High-Performance Link Prediction as a framework for link prediction. They distinguish between two variants:

- HPLP: Does not use the existing unsupervised methods, but only simple Measures like In- and Out-Degree, Max. Flow, Shortest Paths or PropFlow
- HPLP+: Uses the full feature set adding Adamic/Adar, Jaccards coefficient, Katz and Preferential Attachment [2].

2.2.6 Supervised Random Walks

Node and link attributes along with node structure information are used for prediction. Supervised learning strength is assigned to the edges that are likely to have new links in the future so that random walker can visit them more likely. The Strength is not set manually, but learned from the features of each edge and nodes between them.

2.3 META APPROACHES

Meta-Approaches alter the data before being passed to one of the algorithms mentioned above.

2.3.1 Low-rank approximation

For a lot of the mentioned algorithms there is a equivalent formulation for an adjacency matrix M . For a large Matrix M the Matrix M_k is the rank-k matrix, what can be done efficiently by singular value decomposition [9].

- Katz measure using M_k rather than $4MCommonNeighborsscoringbyinnerproductsofrows$ rather than M

The δ contains most related nodes to x under $score(x, .)$ are defined as $S_x^{<\delta>}$. So after calculating the $score(x, y)$, we need to calculate the $S_x^{<\delta>}$.

$$UB(x, y) := |z : z \in \Gamma(y) \cap S_x^{<\delta>}|$$

$$UBw(x, y) := \sum_{z \in \Gamma(y) \cap S_x^{<\delta>}} score(x, z)$$

2.3.2 Clustering

This includes improving the quality of the algorithms by a clustering procedure and after that the algorithm is applied to the modified sub graph. To achieve that the measure is computing $score(x, y)$ for all edge in the original graph and only keeping the p fraction of these edges, where the score is highest [10]. After that the score algorithm is applied to the modified graph. Using this technique, the measurement is only applied to those nodes, in which the scoring algorithm has the most confidence in. This can be seen as a cleaning up by removing of tenuous edges [11].

2.4 Bayesian Probabilistic Model

There are two types of probabilistic approaches to predict links.

The first approach extends a framework of probabilistic relational models capturing probabilistic interactions between attributes of related entities by modelling interactions between the attributes and the link structure itself [12]. For a probability distribution over a database a template describing the relational schema for the domain and the probabilistic dependencies between attributes of the domain in form of a PRM(probabilistic relational model) is specified. Probability distribution on the properties of the nodes and the links can be defined. By including the links into the probabilistic model they can be used to predict other links and to help make predictions about other attributes in the model. If we look at existence uncertainty no assumptions are made about the number of links that exist they are part of the probabilistic model, but can still be used to make inferences about other attributes in the model [13].

The second approach is based on the topological features of network structures only. A probabilistic evolution model of network structure modelling probabilistic flips of existence of edges depending on a copy-and-paste mechanism of edges is presented. Based on this model a transductive learning algorithm for link prediction based on an assumption of the stationarity of the network is proposed. The algorithm realizes a maximum likelihood estimation procedure using exponentiated gradient ascent. This is based on the idea that if a node a has a strong influence on a node b and there is an edge between a and another node c . The authors assume a high probability that a link will establish between b and c and that there is a very low probability that there will never be a node between them [14].

2.5 LINEAR ALGEBRAIC METHOD

It is a general method to solve the link prediction problem which works directly on the graph adjacency matrix or Laplacian matrix. The problem is reduced to a one-dimensional regression problem [9][15, 16]. The training set is reduced to its biggest connected component. The resulting set was then split into two adjacency matrices A and B , where A was the source matrix and B containing one third of

all edges the target matrix. Different curve fitting methods can be used to predict the edge sets in the test set [\[17\]](#).

Chapter 3

Motivation

The node neighbourhood algorithms of link prediction are based on node proximity of a network. Common neighbours, Adamic/Adar index, Jaccard Coefficient, etc. give the friend suggestion by exploiting path length of 2 between the source and his potential friends. As it only considers of path lengths of 2, so it cant give efficient prediction because it only focuses on immediate neighbours of the node. But many other aspects are also needed to predict efficiently. Assuming a node can be connected to others by different paths and of different path lengths, so two nodes which are connected with many unique ways, are more likely to be connected and that varies with the path lengths of different ways in which they are connected. Our Proposed algorithm is more efficient than the algorithms which considers all the paths of the network. Because consideration of all the paths require more time and space complexity. Sometimes it is necessary to get good result with in less interval of time.

Our proposed algorithm performs better than global approaches as it is based on user input bounded path traversal. It predicts the links by traversing to a certain path length given by the user. In global approaches, the time and space complexity are high due to consideration of all paths in the network. As our algorithm only traverse up to certain path length, so its complexity is low with comparison to global approaches. It also outperforms the node neighbourhood algorithms as it traverses more path lengths than the node neighbourhood algorithms. It considers the network characteristics around the target node to predict its future links.

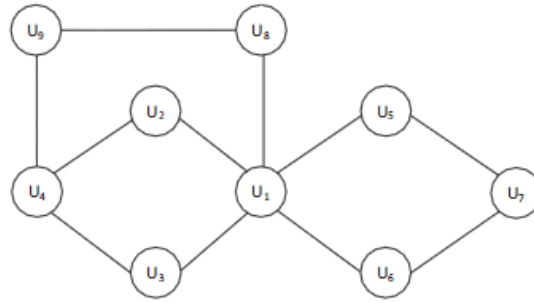


FIGURE 3.1: Link Prediction Problem

When we considers only path lengths of 2, then U_4 and U_7 have the equal probability of forming links with U_1 as they are connected with two different way of path length 2. But when we consider the path length of 3, then U_4 has more

probability to form a link than U_7 . Because U_4 is connect with three different paths with U_1 . If we have followed node neighbourhood techniques, then we will get equal probability of U_4 and U_7 getting connected with U_1 . But through our algorithm with max traversal length of 3, we can conclude that U_4 has more chance to get connected with U_1 than U_7 .

So our algorithm performs better than node neighbourhood algorithms in terms of efficiency of result. It also performs better than global approaches in terms of time and space complexity.

Chapter 4

Proposed Work

The link prediction algorithms based on user input as maximum path to be traversed predicts the probability of formation of link between any two nodes of the network by traversing all the paths of the network up to that certain input path length. It first traverses the path lengths of 2 i.e. the immediate neighbourhoods of the node. we can say it runs a neighbourhood algorithm on path length 2. It then produces a similarity list between every two nodes. When it traverses the graph for path length 3, it uses new paths that are made by path length 2 to get the new path lengths of 3 and computes their similarity matrix and updates the similarity matrix in a cumulative way. This process continues till the graph is traversed up to the maximum path length to be traversed given by user. Let we get a path from A to B while traversing for the path length of $n - 1$ with some similarity value, when we traverse the graph for path length value n , then we will check all the neighbours of B (i.e. C) to get path from A to C . We compute the similarity of each pair (A, C) and update the path list if their no direct link between A and C in the original graph.

The inputs to the algorithm are the graph in terms of a list or adjacency array, the total number of nodes the graph, maximum length to be traversed, which determines how many time the algorithm will run and the path length for each specific traversal. The output of the algorithm is a similarity list containing the similarity value between every two nodes by traversing the path lengths of given maximum user input value. By observing the similarity matrix we can predict the future links. The high similar values have more probability to form links in near future and we can classify the values based on certain threshold value. The similarity values more than the threshold value are likely to form future links. This prediction can be compared with the test data to get the efficiency of the algorithm.

4.1 The Proposed Algorithm

For each path length, we have to follow many steps:

- Calculate that path list with respect to the list with previous input path value
- Update the current adjacency list for the entries having non-zero path value

- Calculate the similarity measure with respect to the corresponding path list
- Update the similarity list by adding the new similarity measures to the list
- Increment the path length

This iteration stops when current path length exceeds the maximum value of path length to be traversed.

4.1.1 Algorithm Parameters

4.1.1.1 Input Parameters

- A : adjacency matrix of undirected and unweighted graph
- n : total number of nodes of the graph
- l : max length of path to be explored in G
- m : the length of a path for current iteration

4.1.1.2 Output Parameters

- $sim(i, j)$: Similarity measure between nodes i and j

4.1.2 Algorithm

Algorithm 1: MAIN FUNCTION

```

for  $m \leftarrow 2$  to  $n$  do
    |  $cpath(A, n, prev, or) \text{ sim} \leftarrow simi(sim, path, n, m);$ 
    |  $path \leftarrow 0$  ;
end

```

The main Program iteratively calls for checking the new collaboration between any two nodes for a specific path length through *cpath* function and computes the

similarity between the new collaborations with exactly m path length and updates the similarity measures through *sim* function.

```

for  $i \leftarrow 1$  to  $N$  do
  for  $j \leftarrow 1$  to  $N$  do
    if  $i < j$  then
      if  $(i,j) \neq j$  then
        for  $k \leftarrow 1$  to  $N$  do
          if  $\text{prev}(i,k) \neq 0$  then
            if  $A(i,k) \neq 0$  and  $(k,j) \neq 0$  then
               $\text{path}(i,j) \leftarrow \text{path}(i,j) + \text{prev}(i,k) * \text{or}(k,j)$  ;
            end
          end
        end
      end
    end
  end
   $\text{path}(j,i) \leftarrow \text{path}(i,j)$  ;
end
end
end
prev  $\leftarrow$  path;
for  $i \leftarrow 1$  to  $N$  do
  for  $j \leftarrow 1$  to  $N$  do
    if  $\text{path}(i,j) \neq 0$  then
       $A(j,i) \leftarrow 1$  ;
    end
  end
end
end
return path and A;

```

The *cpath* function first checks whether there is path from any two nodes of m path length. It checks it by merging the new paths generated while traversing the previous path length $(m - 1)$ and their neighbors in the original graph. So path

matrix contains new collaborations of path length exactly m .

Algorithm 2: FUNCTION SIMI

```

for  $i \leftarrow 1$  to  $n$  do
  for  $j \leftarrow 1$  to  $n$  do
     $\text{lower} \leftarrow 1$ ;
    for  $k \leftarrow 1$  to  $m$  do
       $\text{lower} \leftarrow \text{lower} * (n-k)$  ;
    end
     $\text{sim}(i,j) \leftarrow ( 1/(m-1)* \text{sim}(i,j) ) / \text{lower}$ ;
  end
end
return  $\text{sim}$ ;

```

The *simi* function finds the similarity measure for every pair of nodes which have path length exactly m . It then cumulates the similarity values till the path length of l for every two nodes. The pair of nodes having higher value of similarity are more likely to form link in the near future.

Chapter 5

Data and Experiment Setup

A social network contains nodes and edges represent collaboration between nodes. Suppose we have a snapshot of a social network at a given time. We record multiple interactions between every pair of nodes in different time-stamps. We choose four times $t_0 < t_{00} < t_1 < t_{01}$, and give our algorithm to predict links that are likely to be formed in the near future from the network $G[t_0; t_{00}]$. That results in predicting new links, not present in $G[t_0; t_{00}]$, that are expected to appear in the network $G[t_1; t_{01}]$. We refer to $[t_0; t_{00}]$ as the training interval and $[t_1; t_{01}]$ as the test interval.

As social networks grow very rapidly and exponentially, So there may be may nodes that may not be present in our snapshot of network on which we are predicting. So we will consider only the nodes that are present in our network and their collaborations will be studied. Thus, in evaluating link prediction methods, we will generally use two parameters training set $G[t_0; t_{00}]$ and test set $G[t_1; t_{01}]$. We will then evaluate how accurately the new edges between elements of training set can be predicted.

5.1 Data Sources

5.1.1 Condmat

The first data source is a stream of 19,464 multi-agent events representing condensed matter physics collaborations from 1995 to 2000. We construct weighted, undirected networks from the collaborations by creating a node for each author in the event and a weighted, undirected link connecting each pair of authors. Weights correspond to the number of collaborations two authors share. We use the years 1995 to 1999 (13.9K nodes, 80.6K links) for extracting features as training set and the year 2000 (8.5K nodes, 41.0K links) for obtaining ground truth.

5.1.2 Disease-g

The disease-gene(disease-g) network was constructed from three individual data sets. As the name suggests, this network has two distinct node types, diseases and genes, with four edge types connecting them. It also contains genetic associations, protein -protein interactions, phenotypic links and family links as edges. Here we

have taken a small part of it. The nodes are the diseases and the weights represent the genetic similarity between cancer diseases.

5.2 Network Characteristics

	Condmat	Disease-g
Nodes	17636	1835
Edges	23709	7817
Assortativity Coefficient	0.177	0.31
Avg. Clustering Coefficient	0.642	0.665
Number of SSCs	652	1
Largest SSC	15,081	399
Largest SSC diameter	19	4

Chapter 6

Results and Analysis

6.1 The Evaluation Measures

Let us define P as positive result and N as negative result. The possible outcomes can be formulated in a matrix.

		actual value		
		p	n	total
prediction outcome	p'	True Positive	False Positive	P'
	n'	False Negative	True Negative	N'
total		P	N	

FIGURE 6.1: Confusion matrix

6.1.1 Receiver Operating Characteristic(ROC)

ROC is the variation of true positive rate(TPR) with respect to false positive rate (FPR) at various threshold settings. So it is defined by FPR and TPR as x and y -axis respectively.

TPR = fraction of true positives out of total positives i.e. $TP/P = TP/(TP+FN)$

FPR = fraction of false positives out of total negatives i.e. $FP/N = FP/(FP + TN)$

6.1.2 Precision-Recall Curve

ROC is the variation of Precision with respect to Recall at various threshold settings. So it is defined by Recall and Precision as x and y -axis respectively.

Precision = Positive predictive value i.e. $TP/(TP + FP)$

Recall = fraction of true positives out of total positives i.e. $TP/P = TP/(TP + FN)$

6.2 Comparison between various link Prediction algorithms

There are mainly two types of link prediction algorithms-node neighbourhood techniques and global approaches. We have applied different algorithms to Condmat data set.

6.2.1 ROC curve for Condmat data set

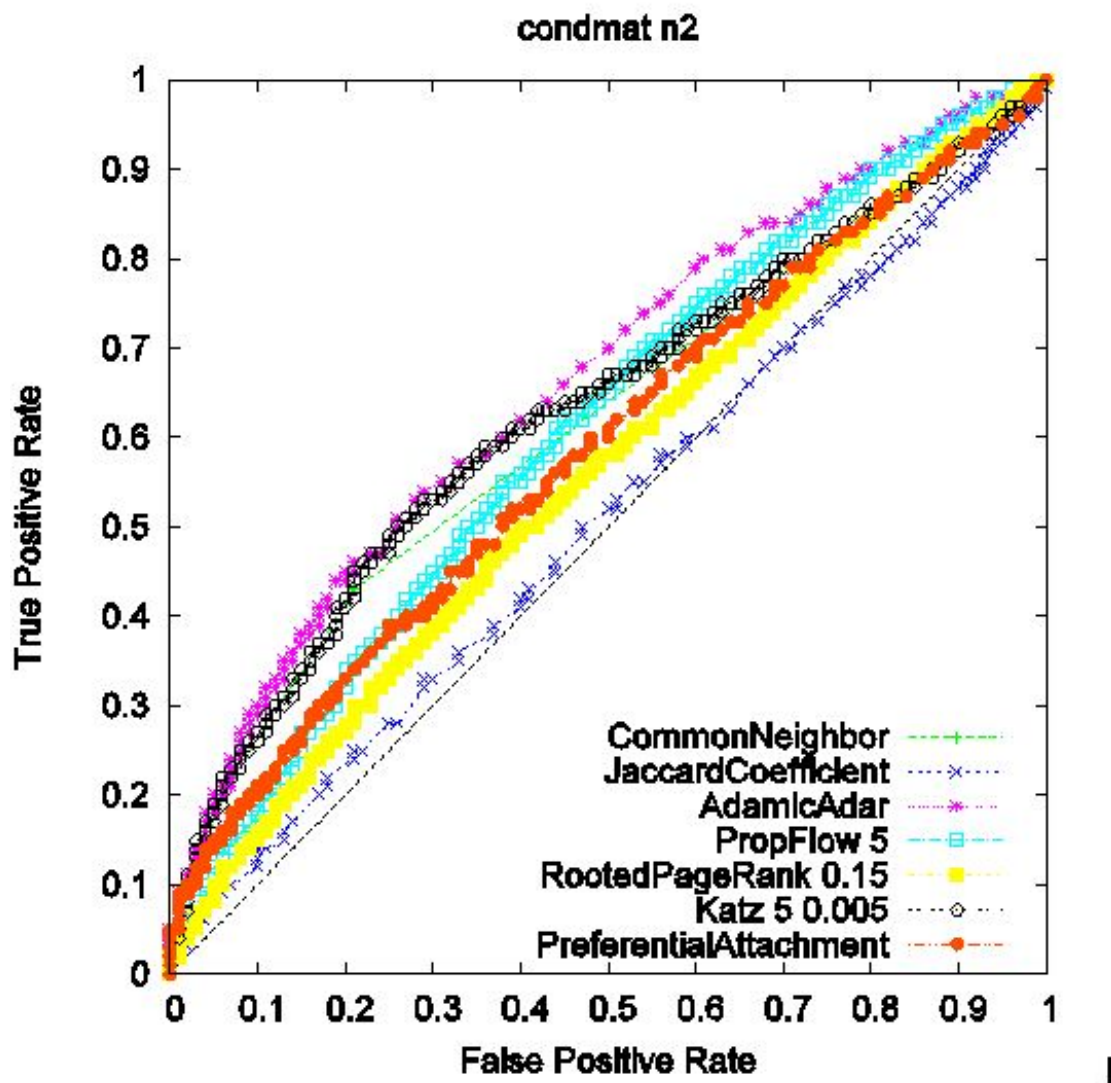


FIGURE 6.2: ROC curve of condmat data

Here we find that Adamic/Adar outperforms the other algorithms.

6.2.2 Precision Recall Curve for Condmat data set

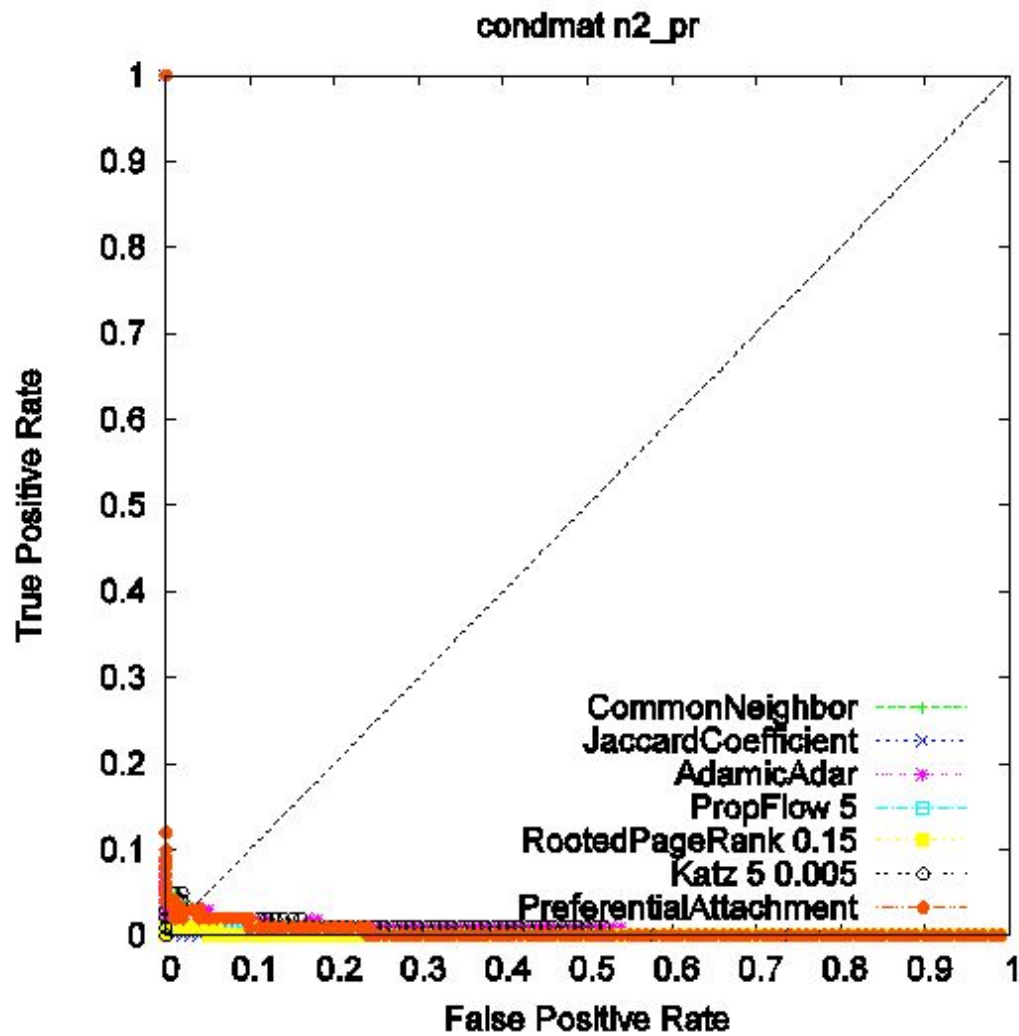


FIGURE 6.3: PR curve of condmat data

Here also we observe that Adamic/Adar outperforms the other algorithms.

6.2.3 ROC curve for Disease-g data set

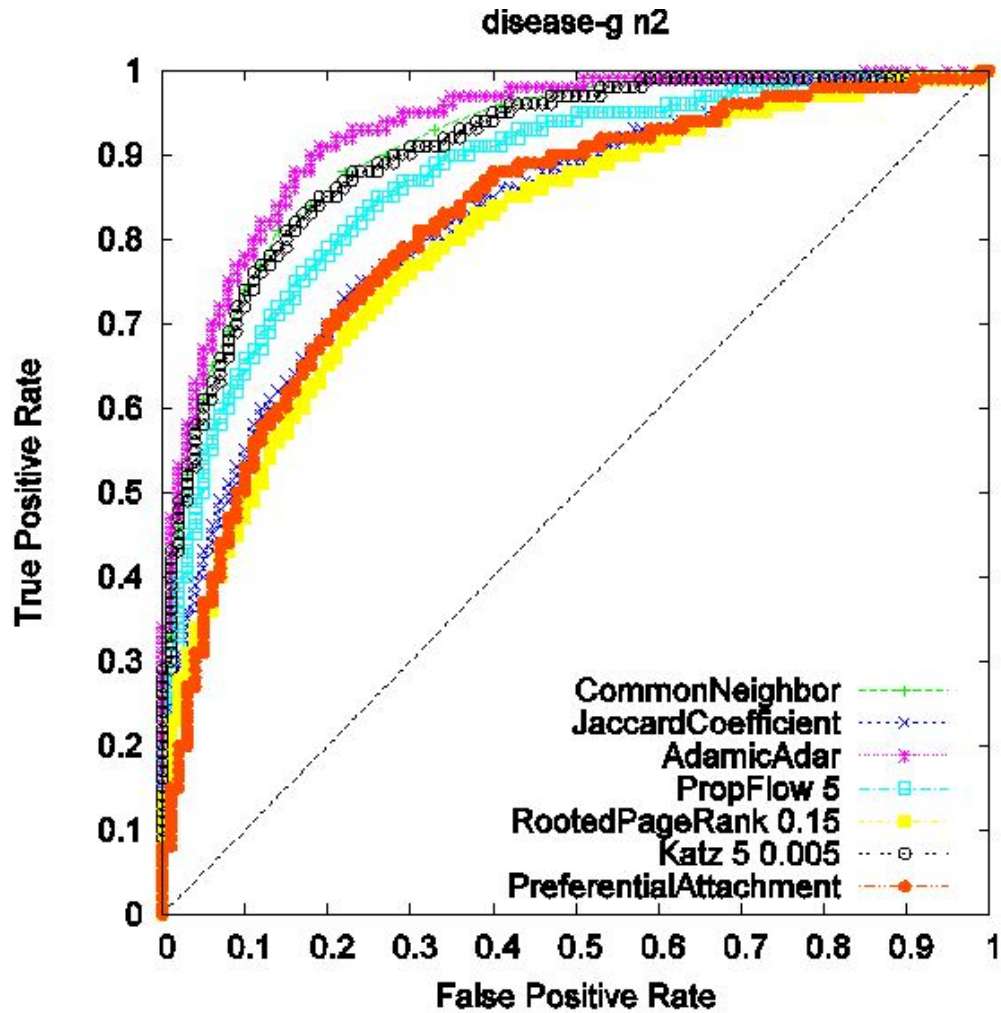


FIGURE 6.4: ROC curve of Disease-g data

Here we find that the result remains the same. Adamic/Adar performs well with comparison to the other algorithms.

6.2.4 Precision Recall Curve for Disease-g data set

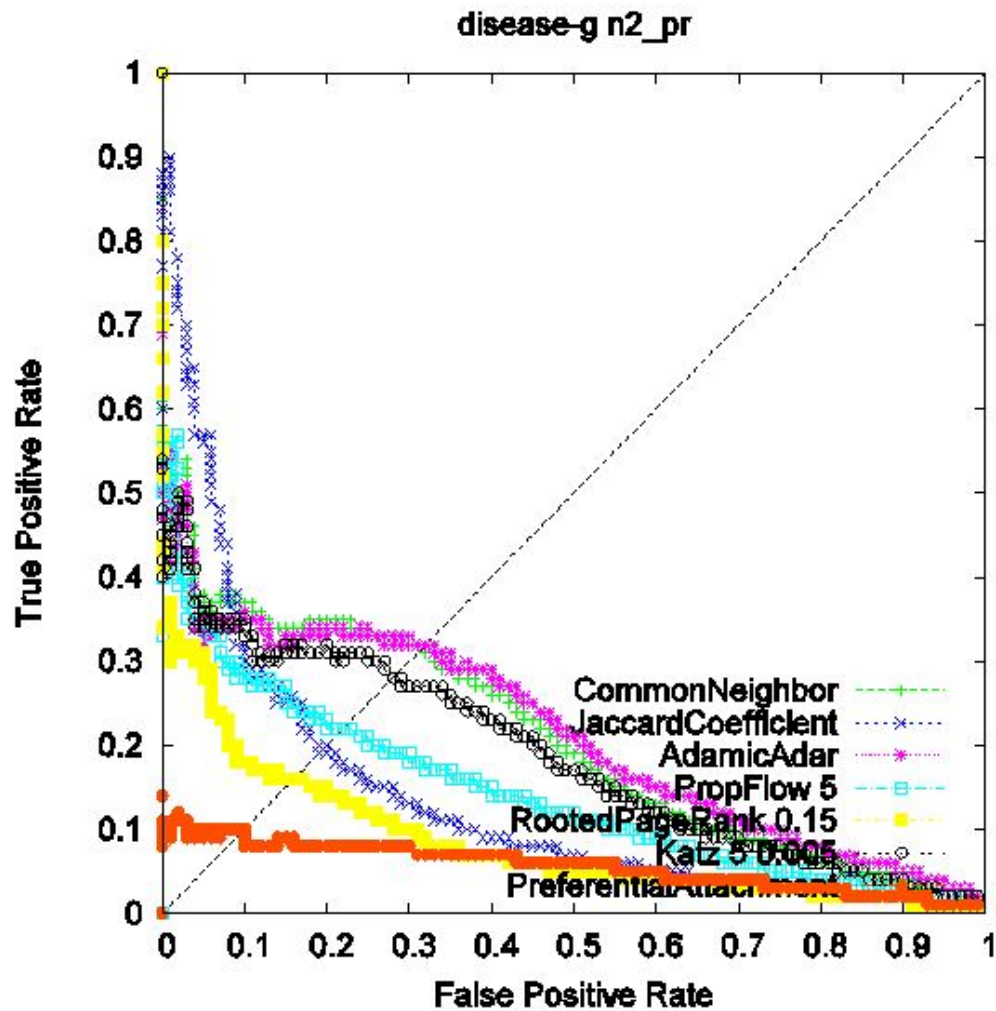


FIGURE 6.5: PR curve of Disease-g data

Adamic/Adar is the best and most stable graph proximity measurement of the unweighted node neighbourhood based algorithms in almost all categories when it doesn't score highest, the difference is not much.

6.3 Our Proposed Method Implementation

We are implementing our proposed method on a small network. The input to the algorithms is the network below and the output is a similarity matrix. It has been discussed that with path length of 3, U_4 has more probability to form link with U_1 with comparison to U_7 .

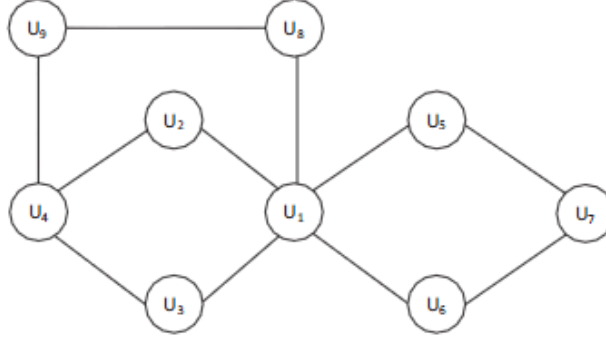


FIGURE 6.6: Link Prediction Analysis

The algorithm is implemented using maximum length to be traversed as 4. This result shows that the similarity value of the node pair U_1 and U_4 is maximum

```
sim =
```

0	0	0	0.3013	0	0	0.2857	0	0.1690
0	0	0.2857	0	0.1466	0.1466	0.0253	0.1568	0.1568
0	0.2857	0	0	0.1466	0.1466	0.0253	0.1568	0.1568
0.3013	0	0	0	0.0281	0.0281	0.0089	0.1690	0
0	0.1466	0.1466	0.0281	0	0.2857	0	0.1456	0.0171
0	0.1466	0.1466	0.0281	0.2857	0	0	0.1456	0.0171
0.2857	0.0253	0.0253	0.0089	0	0	0	0.0253	0.0055
0	0.1568	0.1568	0.1690	0.1456	0.1456	0.0253	0	0
0.1690	0.1568	0.1568	0	0.0171	0.0171	0.0055	0	0

```
>>
```

FIGURE 6.7: Similarity matrix

and more than that of the pair U_1 and U_7 . So, there is more probability of formation of link between U_1 and U_4 . Hence our proposed method works correctly.

6.4 Complexity Analysis

Global approaches traverses all paths of the network to predict the links. They require matrix inversion. So the time complexity for global techniques is $O(n^3)$.

The node neighborhood approaches traverses path length of 2 in a network. That means, for any node it first traverses all its neighbors and then their neighbors and computes the similarity of the source node with its neighbors neighbor. Let h be the average node degree of the network. As $h \ll n$, so the time complexity is $(n \cdot h^2)$. As our method is based on bounded length traversal, it traverses up to a path length of l . So the time complexity is $O(n \cdot h^l)$ and the space complexity is $O(n \cdot h)$. So Our method is better than global approaches in terms of complexity.

	Condmat	Disease-g
Page Rank	370 sec	530 sec
katz	430 sec	620 sec
Node neighbor	72 sec	230 sec
Proposed	260 sec	350 sec

This result shows that our algorithm takes less time as compared to the global approaches. Node neighbor approach is taking less time as it focuses on only immediate surroundings of the node and traverse only paths of length 2.

The below figure shows the bar plot of the time taken by different algorithms and the proposed algorithms.

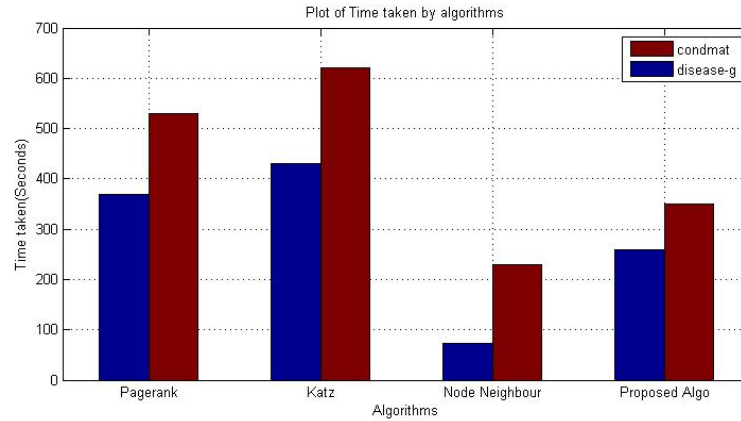


FIGURE 6.8: Bar Plot of Time takes by algorithms

Chapter 7

Conclusions and Future Works

7.1 Conclusions

Link Prediction is the method to predict the possible future interactions among the nodes in the near future. Our algorithm uses both global and local characteristics of the network to predict the links. Global approaches has the time constraint as they traverse all paths of network to predict the links and local approaches are less efficient as they consider only local features of the node. Our approach is compared with all the approaches and it provides efficient and accurate friend suggestions in a less interval of time

7.2 Future Research Opportunities

Link Prediction based on other features like photo, video tagging can be used for better prediction. As many features as we consider simultaneously, the prediction will be better because it gives information about many ways peoples may by connected. We can consider the positive as well as negative links in a network. If positive weight is for support, then negative weight should be for opposing it. As network is always dynamic, so we can consider network dynamics into consideration.

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